



- 1 -

# SEQUENCE LISTING

<110> Pawlowski, Krzysztof  
Reed, John C.  
Godzik, Adam

<120> CARD-DOMAIN CONTAINING POLYPEPTIDES,  
ENCODING NUCLEIC ACIDS, AND METHODS OF USE

<130> P-LJ 5100

<140> US 10/032,159

<141> 2001-12-19

<150> US 60/257,457

<151> 2000-12-21

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1101

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1101)

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ttc	cgg	gtg	acg	ctc	acc	tcg	gtc	atc	gac	ccc	tca	cgc	atc	aca	cct	96
Phe	Arg	Val	Thr	Leu	Thr	Ser	Val	Ile	Asp	Pro	Ser	Arg	Ile	Thr	Pro	
			20					25					30			

tac	ctg	cgg	cag	tgc	aag	gtc	ctg	aac	cct	gat	gat	gag	gag	cag	gtg	144
Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln	Val	
			35				40					45				

ctc	agc	gac	ccc	aac	ctg	gtc	atc	cgc	aaa	cgg	aaa	gtg	ggt	gtg	ctc	192
Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val	Leu	
			50				55					60				

ctg	gac	atc	ctg	cag	cgg	acc	ggc	cac	aag	ggc	tac	gtg	gcc	ttc	ctc	240
Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe	Leu	
			65				70					75				80

gag agc ctg gag ctc tac tac ccg cag ctg tac aag aag gtc aca ggc	288
Glu Ser Leu Glu Leu Tyr Tyr Pro Gln Leu Tyr Lys Lys Val Thr Gly	
85 90 95	
aag gag ccg gcc cgc gtc ttc tcc atg atc atc gac gcg tcc ggg gag	336
Lys Glu Pro Ala Arg Val Phe Ser Met Ile Ile Asp Ala Ser Gly Glu	
100 105 110	
tca ggc ctg act cag ctg ctg atg act gag gtc atg aag ctg cag aag	384
Ser Gly Leu Thr Gln Leu Leu Met Thr Glu Val Met Lys Leu Gln Lys	
115 120 125	
aag gtg cag gac ctg acc gcg ctg ctg agc tcc aaa gat gac ttc atc	432
Lys Val Gln Asp Leu Thr Ala Leu Leu Ser Ser Lys Asp Asp Phe Ile	
130 135 140	
aag gag ctg cgg gtg aag gac agc ctg ctg cgc aag cac cag gag cgt	480
Lys Glu Leu Arg Val Lys Asp Ser Leu Leu Arg Lys His Gln Glu Arg	
145 150 155 160	
gtg cag agg ctc aag gag gag tgc gag gcc ggc agc cgc gag ctc aag	528
Val Gln Arg Leu Lys Glu Glu Cys Glu Ala Gly Ser Arg Glu Leu Lys	
165 170 175	
cgc tgc aag gag gag aac tac gac ctg gcc atg cgc ctg gcg cac cag	576
Arg Cys Lys Glu Glu Asn Tyr Asp Leu Ala Met Arg Leu Ala His Gln	
180 185 190	
agt gag gag aag ggc gcc gcg ctc atg cgg aac cgt gac ctg cag ctg	624
Ser Glu Glu Lys Gly Ala Ala Leu Met Arg Asn Arg Asp Leu Gln Leu	
195 200 205	
gag att gac cag ctc aag cac agc ctc atg aag gcc gag gac gac tgc	672
Glu Ile Asp Gln Leu Lys His Ser Leu Met Lys Ala Glu Asp Asp Cys	
210 215 220	
aag gtg gag cgc aag cac acg ctg aag ctc agg cac gcc atg gag cag	720
Lys Val Glu Arg Lys His Thr Leu Lys Leu Arg His Ala Met Glu Gln	
225 230 235 240	
cgg ccc agc cag gag ctg ctg tgg gag ctg cag cag gag aag gcc ctg	768
Arg Pro Ser Gln Glu Leu Leu Trp Glu Leu Gln Gln Glu Lys Ala Leu	
245 250 255	
ctc cag gcc cgg gtg cag gag ctg gag gcc tcc gtc cag gag ggg aag	816
Leu Gln Ala Arg Val Gln Glu Leu Glu Ala Ser Val Gln Glu Gly Lys	
260 265 270	
ctg gac agg agc agc ccc tac atc cag gta ctg gag gag gac tgg cgg	864
Leu Asp Arg Ser Ser Pro Tyr Ile Gln Val Leu Glu Glu Asp Trp Arg	
275 280 285	
cag gcg ctg cgg gac cac cag gag cag gcc aac acc atc ttc tcc ctg	912

Gln	Ala	Leu	Arg	Asp	His	Gln	Glu	Gln	Ala	Asn	Thr	Ile	Phe	Ser	Leu	
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cgc	aag	gac	ctc	cgc	cag	ggc	gag	gcc	cga	cgc	ctc	cgg	tgc	atg	gag	960
Arg	Lys	Asp	Leu	Arg	Gln	Gly	Glu	Ala	Arg	Arg	Leu	Arg	Cys	Met	Glu	
305					310					315					320	
gag	aag	gag	atg	ttc	gag	ctg	cag	tgc	ctg	gca	cta	cgt	aag	gac	tcc	1008
Glu	Lys	Glu	Met	Phe	Glu	Leu	Gln	Cys	Leu	Ala	Leu	Arg	Lys	Asp	Ser	
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aag	atg	tac	aag	gac	cgc	atc	gag	gcc	atc	ctg	ctg	cag	atg	gag	gag	1056
Lys	Met	Tyr	Lys	Asp	Arg	Ile	Glu	Ala	Ile	Leu	Leu	Gln	Met	Glu	Glu	
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gtc	gcc	att	gag	cgg	gac	cag	agc	aca	caa	atg	gag	ggg	ctg	tga		1101
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<400> 2

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Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln	Val	
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Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val	Leu	
	50				55					60						
Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe	Leu	
65				70					75						80	
Glu	Ser	Leu	Glu	Leu	Tyr	Tyr	Pro	Gln	Leu	Tyr	Lys	Lys	Val	Thr	Gly	
			85					90						95		
Lys	Glu	Pro	Ala	Arg	Val	Phe	Ser	Met	Ile	Ile	Asp	Ala	Ser	Gly	Glu	
		100						105					110			
Ser	Gly	Leu	Thr	Gln	Leu	Leu	Met	Thr	Glu	Val	Met	Lys	Leu	Gln	Lys	
	115					120						125				
Lys	Val	Gln	Asp	Leu	Thr	Ala	Leu	Leu	Ser	Ser	Lys	Asp	Asp	Phe	Ile	
	130					135					140					
Lys	Glu	Leu	Arg	Val	Lys	Asp	Ser	Leu	Leu	Arg	Lys	His	Gln	Glu	Arg	
145				150						155					160	
Val	Gln	Arg	Leu	Lys	Glu	Glu	Cys	Glu	Ala	Gly	Ser	Arg	Glu	Leu	Lys	
			165					170						175		
Arg	Cys	Lys	Glu	Asn	Tyr	Asp	Leu	Ala	Met	Arg	Leu	Ala	His	Gln		
		180					185					190				
Ser	Glu	Glu	Lys	Gly	Ala	Ala	Leu	Met	Arg	Asn	Arg	Asp	Leu	Gln	Leu	
	195					200						205				

Glu Ile Asp Gln Leu Lys His Ser Leu Met Lys Ala Glu Asp Asp Cys  
 210 215 220  
 Lys Val Glu Arg Lys His Thr Leu Lys Leu Arg His Ala Met Glu Gln  
 225 230 235 240  
 Arg Pro Ser Gln Glu Leu Leu Trp Glu Leu Gln Gln Glu Lys Ala Leu  
 245 250 255  
 Leu Gln Ala Arg Val Gln Glu Leu Glu Ala Ser Val Gln Glu Gly Lys  
 260 265 270  
 Leu Asp Arg Ser Ser Pro Tyr Ile Gln Val Leu Glu Glu Asp Trp Arg  
 275 280 285  
 Gln Ala Leu Arg Asp His Gln Glu Gln Ala Asn Thr Ile Phe Ser Leu  
 290 295 300  
 Arg Lys Asp Leu Arg Gln Gly Glu Ala Arg Arg Leu Arg Cys Met Glu  
 305 310 315 320  
 Glu Lys Glu Met Phe Glu Leu Gln Cys Leu Ala Leu Arg Lys Asp Ser  
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 tca cgc atc aca cct tac ctg cgg cag tgc aag gtc ctg aac cct gat 96  
 Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp  
 20 25 30  
 gat gag gag cag gtg ctc agc gac ccc aac ctg gtc atc cgc aaa cgg 144  
 Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg  
 35 40 45  
 aaa gtg ggt gtg ctc ctg gac atc ctg cag cgg acc ggc cac aag ggc 192  
 Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly  
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 tac gtg gcc ttc ctc gag agc ctg 216  
 Tyr Val Ala Phe Leu Glu Ser Leu  
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 <213> Homo sapiens

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 Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn Pro Asp  
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 Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg Lys Arg  
 35 40 45  
 Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His Lys Gly  
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 Tyr Val Ala Phe Leu Glu Ser Leu  
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<220>  
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 gcc ggc agc cgc gag ctc aag cgc tgc aag gag gag aac tac gac ctg 96  
 Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu  
 20 25 30  
 gcc atg cgc ctg gcg cac cag agt gag gag aag ggc gcc gcg ctc atg 144  
 Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met  
 35 40 45  
 cgg aac cgt gac ctg cag ctg gag att gac cag ctc aag cac agc ctc 192  
 Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu  
 50 55 60  
 atg aag gcc gag gac gac tgc aag gtg gag cgc aag cac acg ctg aag 240  
 Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys  
 65 70 75 80  
 ctc agg cac gcc atg gag cag cgg ccc agc cag gag ctg ctg tgg gag 288  
 Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu  
 85 90 95  
 ctg cag cag gag aag gcc ctg ctc cag gcc cgg gtg cag gag ctg gag 336

Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu  
100 105 110

gcc tcc gtc cag gag ggg aag ctg gac agg agc agc ccc tac atc cag 384  
Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln  
115 120 125

gta ctg gag gag gac tgg cgg cag gcg ctg cgg gac cac cag gag cag 432  
Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln  
130 135 140

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<212> PRT

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35 40 45  
Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu  
50 55 60  
Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys  
65 70 75 80  
Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu  
85 90 95  
Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu  
100 105 110  
Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln  
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Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln  
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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)... (3744)

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gag aat gtg gag tgt aac cgg cac atg ctc agc cgc tat atc aac cct	96
Glu Asn Val Glu Cys Asn Arg His Met Leu Ser Arg Tyr Ile Asn Pro	
20 25 30	
gcc aag ctc acg ccc tac ctg cgt cag tgt aag gtc att gat gag cag	144
Ala Lys Leu Thr Pro Tyr Leu Arg Gln Cys Lys Val Ile Asp Glu Gln	
35 40 45	
gat gaa gat gaa gtg ctt aat gcc cct atg ctg cca tcc aag atc aac	192
Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu Pro Ser Lys Ile Asn	
50 55 60	
cga gca ggc cgg ctg ttg gac att cta cat acc aag ggg caa agg ggc	240
Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr Lys Gly Gln Arg Gly	
65 70 75 80	
tat gtg gtc ttc ttg gag agc cta gaa ttt tat tac cca gaa ctg tac	288
Tyr Val Val Phe Leu Glu Ser Leu Glu Phe Tyr Tyr Pro Glu Leu Tyr	
85 90 95	
aaa ctg gtg act ggg aaa gag ccc act cgg aga ttc tcc acc att gtg	336
Lys Leu Val Thr Gly Lys Glu Pro Thr Arg Arg Phe Ser Thr Ile Val	
100 105 110	
gtg gag gaa ggc cac gag ggc ctc acg cac ttc ctg atg aac gag gtc	384
Val Glu Glu Gly His Glu Gly Leu Thr His Phe Leu Met Asn Glu Val	
115 120 125	
atc aag ctg cag cag cag atg aag gcc aag gac ctg caa cgc tgc gag	432
Ile Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu	
130 135 140	
ctg ctg gcc agg ttg cgg cag ctg gag gat gag aag aag cag atg acg	480
Leu Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr	
145 150 155 160	
ctg acg cgc gtg gag ctg cta acc ttc cag gag cgg tac tac aag atg	528
Leu Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met	
165 170 175	
aag gaa gag cgg gac agc tac aat gac gag ctg gtc aag gtg aag gac	576
Lys Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp	
180 185 190	
gac aac tac aac tta gcc atg cgc tac gca cag ctc agt gag gag aag	624
Asp Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys	
195 200 205	
aac atg gcg gtc atg agg agc cga gac ctc caa ctc gag atc gat cag	672
Asn Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu Glu Ile Asp Gln	
210 215 220	
cta aag cac cgg ttg aat aag atg gag gag gaa tgt aag ctg gag aga	720

Leu Lys His Arg Leu Asn Lys Met Glu Glu Glu Cys Lys Leu Glu Arg	
225 230 235 240	
aat cag tct cta aaa ctg aag aat gac att gaa aat cgg ccc aag aag	768
Asn Gln Ser Leu Lys Leu Lys Asn Asp Ile Glu Asn Arg Pro Lys Lys	
245 250 255	
gag cag gtt ctg gaa ctg gag cgg gag aat gaa atg ctg aag acc aaa	816
Glu Gln Val Leu Glu Leu Glu Arg Glu Asn Glu Met Leu Lys Thr Lys	
260 265 270	
aac cag gag ctg cag tcc atc atc cag gcc ggg aag cgc agc ctg cca	864
Asn Gln Glu Leu Gln Ser Ile Ile Gln Ala Gly Lys Arg Ser Leu Pro	
275 280 285	
gac tca gac aag gcc atc ctg gac atc ttg gaa cac gac cgc aag gag	912
Asp Ser Asp Lys Ala Ile Leu Asp Ile Leu Glu His Asp Arg Lys Glu	
290 295 300	
gcc ctg gag gac agg cag gag ctg gtc aac agg atc tac aac ctg cag	960
Ala Leu Glu Asp Arg Gln Glu Leu Val Asn Arg Ile Tyr Asn Leu Gln	
305 310 315 320	
gag gag gcc cgc cag gca gag gag ctg cga gac aag tac ctg gag gag	1008
Glu Glu Ala Arg Gln Ala Glu Glu Leu Arg Asp Lys Tyr Leu Glu Glu	
325 330 335	
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Lys Glu Asp Leu Glu Leu Lys Cys Ser Thr Leu Gly Lys Asp Cys Glu	
340 345 350	
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Met Tyr Lys His Arg Met Asn Thr Val Met Leu Gln Leu Glu Glu Val	
355 360 365	
gag cgg gag cgg gac cag gga cag gct gtg gcc ttc cag gga cac tgc	1152
Glu Arg Glu Arg Asp Gln Gly Gln Ala Val Ala Phe Gln Gly His Cys	
370 375 380	
atc aaa gct ctc aac aca gag cct gcc act agc aag ggt cgg acc atc	1200
Ile Lys Ala Leu Asn Thr Glu Pro Ala Thr Ser Lys Gly Arg Thr Ile	
385 390 395 400	
ggc tct gtg atc gcg tta atg aag aag gcc ttc cac tcc cga gat gaa	1248
Gly Ser Val Ile Ala Leu Met Lys Lys Ala Phe His Ser Arg Asp Glu	
405 410 415	
gct cag aca cag tac tcg cag tgc tta atc gaa aag gac aag tac agg	1296
Ala Gln Thr Gln Tyr Ser Gln Cys Leu Ile Glu Lys Asp Lys Tyr Arg	
420 425 430	
aag cag atc cgc gag ctg gag gag aag aac gac gag atg agg atc gag	1344
Lys Gln Ile Arg Glu Leu Glu Glu Lys Asn Asp Glu Met Arg Ile Glu	



435	440	445	
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gaa gac agc aag tac ttc ctg ccc tac cat ccg ccc cag cgc agg atg Glu Asp Ser Lys Tyr Phe Leu Pro Tyr His Pro Pro Gln Arg Arg Met 515 520 525			1584
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gac gcc agc cct agc tcc tgc gga tct ctg ccc atc acc aac tcc ttc Asp Ala Ser Pro Ser Ser Cys Gly Ser Leu Pro Ile Thr Asn Ser Phe 565 570 575			1728
acc aag atg ccc ccc cgg agc cgc agc agc atc atg tca atc acc gcc Thr Lys Met Pro Pro Arg Ser Arg Ser Ser Ile Met Ser Ile Thr Ala 580 585 590			1776
gag ccc ccg gga aac gac tcc atc gtc aga cgc tac aag gag gac gcg Glu Pro Pro Gly Asn Asp Ser Ile Val Arg Arg Tyr Lys Glu Asp Ala 595 600 605			1824
ccc cat cgc agc aca gtc gaa gaa gac aat gac agc ggc ggg ttt gac Pro His Arg Ser Thr Val Glu Glu Asp Asn Asp Ser Gly Gly Phe Asp 610 615 620			1872
gcc tta gat ctg gat gag ctg gca gca ggg gag act gtg gct cag agt Ala Leu Asp Leu Asp Glu Leu Ala Ala Gly Glu Thr Val Ala Gln Ser 625 630 635 640			1920
cct cca ggt gtg ccc tgc cag ccc cct ctc ttc cag ggc tcc ccc agc Pro Pro Gly Val Pro Cys Gln Pro Pro Leu Phe Gln Gly Ser Pro Ser 645 650 655			1968

ctt tgc cag cta agg ctg cca acc gat gaa acg aaa gat gag tgg tcc	2016
Leu Cys Gln Leu Arg Leu Pro Thr Asp Glu Thr Lys Asp Glu Trp Ser	
660 665 670	
tcc tta atg ggg aag cat cag cgc tac caa gtg tta aag aga gat gac	2064
Ser Leu Met Gly Lys His Gln Arg Tyr Gln Val Leu Lys Arg Asp Asp	
675 680 685	
agt cac gaa cgc tac tcc ttc gga ccc tcc tcc atc cac tcc tcc tcc	2112
Ser His Glu Arg Tyr Ser Phe Gly Pro Ser Ser Ile His Ser Ser Ser	
690 695 700	
tcc tcc cac caa tcc gag ggc ctg gat gcc tac gac ctg gag cag gtc	2160
Ser Ser His Gln Ser Glu Gly Leu Asp Ala Tyr Asp Leu Glu Gln Val	
705 710 715 720	
aac ctc atg ttc agg aag ttc tct ctg gaa aga ccc ttc cgg cct tcg	2208
Asn Leu Met Phe Arg Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser	
725 730 735	
gtc acc tct gtg ggg cac gtg cgg ggc cca ggg ccc tcg gtg cag cac	2256
Val Thr Ser Val Gly His Val Arg Gly Pro Gly Pro Ser Val Gln His	
740 745 750	
acg acg ctg aat ggc gac agc ctc acc tcc cag ctc acc ctg ctg ggg	2304
Thr Thr Leu Asn Gly Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly	
755 760 765	
ggc aac gcg cga ggg agc ttc gtg cac tcg gtc aag cct ggc tct ctg	2352
Gly Asn Ala Arg Gly Ser Phe Val His Ser Val Lys Pro Gly Ser Leu	
770 775 780	
gcc gag aaa gcc ggc ctc cgt gag ggc cac cag ctg ctg ctg cta gaa	2400
Ala Glu Lys Ala Gly Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu	
785 790 795 800	
ggc tgc atc cga ggc gag agg cag agt gtc ccg ttg gac aca tgc acc	2448
Gly Cys Ile Arg Gly Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr	
805 810 815	
aaa gag gaa gcc cac tgg acc atc cag agg tgc agc ggc ccc gtc acg	2496
Lys Glu Glu Ala His Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr	
820 825 830	
ctg cac tac aag gtc aac cac gaa gcc cag cag aaa atc cgt ggg cct	2544
Leu His Tyr Lys Val Asn His Glu Ala Gln Gln Lys Ile Arg Gly Pro	
835 840 845	
gca gaa tat gat gtg ggc agc acc tcc aaa gcc cgg agc tgc gca gca	2592
Ala Glu Tyr Asp Val Gly Ser Thr Ser Lys Ala Arg Ser Cys Ala Ala	
850 855 860	

gca cag ccc tgc aag tct gga att cca ggg aaa gaa agt tca ttc cgg	2640
Ala Gln Pro Cys Lys Ser Gly Ile Pro Gly Lys Glu Ser Ser Phe Arg	
865 870 875 880	
cag ggg tac cgg aag ctg gtg aag gac atg gag gac ggc ctg atc aca	2688
Gln Gly Tyr Arg Lys Leu Val Lys Asp Met Glu Asp Gly Leu Ile Thr	
885 890 895	
tcg ggg gac tcg ttc tac atc cgg ctg aac ctg aac atc tcc agc cag	2736
Ser Gly Asp Ser Phe Tyr Ile Arg Leu Asn Leu Asn Ile Ser Ser Gln	
900 905 910	
ctg gac gcc tgc acc atg tcc ctg aag tgt gac gat gtt gtg cac gtc	2784
Leu Asp Ala Cys Thr Met Ser Leu Lys Cys Asp Asp Val Val His Val	
915 920 925	
cgt gac acc atg tac cag gac agg cac gag tgg ctg tgc gcg cgg gtc	2832
Arg Asp Thr Met Tyr Gln Asp Arg His Glu Trp Leu Cys Ala Arg Val	
930 935 940	
gac cct ttc aca gac cat gac ctg gat atg ggc acc ata ccc agc tac	2880
Asp Pro Phe Thr Asp His Asp Leu Asp Met Gly Thr Ile Pro Ser Tyr	
945 950 955 960	
agc cga gcc cag cag ctc ctc ctg gtg aaa ctg cag cgc ctg atg cac	2928
Ser Arg Ala Gln Gln Leu Leu Leu Val Lys Leu Gln Arg Leu Met His	
965 970 975	
cga ggc agc cgg gag gag gta gac ggc acc cac cac acc ctg cgg gca	2976
Arg Gly Ser Arg Glu Glu Val Asp Gly Thr His His Thr Leu Arg Ala	
980 985 990	
ctc cgg ttc gtc agc agg tcc gag aac aag tat aag cgg atg aac agc	3024
Leu Arg Phe Val Ser Arg Ser Glu Asn Lys Tyr Lys Arg Met Asn Ser	
995 1000 1005	
aat gag cgg gtc cgc atc atc tcg ggg agt ccg cta ggg agc ctg gcc	3072
Asn Glu Arg Val Arg Ile Ile Ser Gly Ser Pro Leu Gly Ser Leu Ala	
1010 1015 1020	
cgg tcc tcg ctg gac gcc acc aag ctc ttg act gag aag cag gaa gag	3120
Arg Ser Ser Leu Asp Ala Thr Lys Leu Leu Thr Glu Lys Gln Glu Glu	
1025 1030 1035 1040	
ctg gac cct gag agc gag ctg ggc aag aac ctc agc ctc atc ccc tac	3168
Leu Asp Pro Glu Ser Glu Leu Gly Lys Asn Leu Ser Leu Ile Pro Tyr	
1045 1050 1055	
agc ctg gta cgc gcc ttc tac tgc gag cgc cgc cgg ccc gtg ctc ttc	3216
Ser Leu Val Arg Ala Phe Tyr Cys Glu Arg Arg Arg Pro Val Leu Phe	
1060 1065 1070	
aca ccc acc gtg ctg gcc aag acg ctg gtg cag agg ctg ctc aac tcg	3264

Thr	Pro	Thr	Val	Leu	Ala	Lys	Thr	Leu	Val	Gln	Arg	Leu	Leu	Asn	Ser		
	1075						1080					1085					
gga	ggt	gcc	atg	gag	ttc	acc	atc	tgc	aag	tca	gat	atc	gtc	aca	aga	3312	
Gly	Gly	Ala	Met	Glu	Phe	Thr	Ile	Cys	Lys	Ser	Asp	Ile	Val	Thr	Arg		
	1090					1095				1100							
gat	gag	ttc	ctc	aga	agg	cag	aag	acg	gag	acc	atc	atc	tac	tcc	cga	3360	
Asp	Glu	Phe	Leu	Arg	Arg	Gln	Lys	Thr	Glu	Thr	Ile	Ile	Tyr	Ser	Arg		
1105				1110				1115					1120				
gag	aag	aac	ccc	aac	gcg	ttc	gaa	tgc	atc	gcc	cct	gcc	aac	att	gaa	3408	
Glu	Lys	Asn	Pro	Asn	Ala	Phe	Glu	Cys	Ile	Ala	Pro	Ala	Asn	Ile	Glu		
			1125					1130					1135				
gct	gtg	gcc	gcc	aag	aac	aag	cac	tgc	ctg	ctg	gag	gct	ggg	atc	ggc	3456	
Ala	Val	Ala	Ala	Lys	Asn	Lys	His	Cys	Leu	Leu	Glu	Ala	Gly	Ile	Gly		
			1140					1145					1150				
tgc	aca	aga	gac	ttg	atc	aag	tcc	aac	atc	tac	ccc	atc	gtg	ctc	ttc	3504	
Cys	Thr	Arg	Asp	Leu	Ile	Lys	Ser	Asn	Ile	Tyr	Pro	Ile	Val	Leu	Phe		
	1155					1160						1165					
atc	cgg	gtg	tgt	gag	aag	aac	atc	aag	agg	ttc	aga	aag	ctg	ctg	ccc	3552	
Ile	Arg	Val	Cys	Glu	Lys	Asn	Ile	Lys	Arg	Phe	Arg	Lys	Leu	Leu	Pro		
	1170					1175				1180							
cgg	cct	gag	acg	gag	gag	gag	ttc	ctg	cgc	gtg	tgc	cgg	ctg	aag	gag	3600	
Arg	Pro	Glu	Thr	Glu	Glu	Glu	Phe	Leu	Arg	Val	Cys	Arg	Leu	Lys	Glu		
1185				1190				1195					1200				
aag	gag	ctg	gag	gcc	ctg	ccg	tgc	ctg	tac	gcc	acg	gtg	gaa	cct	gac	3648	
Lys	Glu	Leu	Glu	Ala	Leu	Pro	Cys	Leu	Tyr	Ala	Thr	Val	Glu	Pro	Asp		
			1205					1210					1215				
atg	tgg	ggc	agc	gta	gag	gag	ctg	ctc	cgc	gtt	gtc	aag	gac	aag	atc	3696	
Met	Trp	Gly	Ser	Val	Glu	Glu	Leu	Leu	Arg	Val	Val	Lys	Asp	Lys	Ile		
			1220					1225					1230				
ggc	gag	gag	cag	cgc	aag	acc	atc	tgg	gtg	gac	gag	gac	cag	ctg	tga	3744	
Gly	Glu	Glu	Gln	Arg	Lys	Thr	Ile	Trp	Val	Asp	Glu	Asp	Gln	Leu	*		
	1235							1240					1245				

<210> 8

<211> 1247

<212> PRT

<213> Homo sapiens

<400> 8

Met	Asp	Asp	Tyr	Met	Glu	Thr	Leu	Lys	Asp	Glu	Glu	Asp	Ala	Leu	Trp
1				5				10						15	

Glu	Asn	Val	Glu	Cys	Asn	Arg	His	Met	Leu	Ser	Arg	Tyr	Ile	Asn	Pro	20	25	30
Ala	Lys	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Cys	Lys	Val	Ile	Asp	Glu	Gln	35	40	45
Asp	Glu	Asp	Glu	Val	Leu	Asn	Ala	Pro	Met	Leu	Pro	Ser	Lys	Ile	Asn	50	55	60
Arg	Ala	Gly	Arg	Leu	Leu	Asp	Ile	Leu	His	Thr	Lys	Gly	Gln	Arg	Gly	65	70	75
Tyr	Val	Val	Phe	Leu	Glu	Ser	Leu	Glu	Phe	Tyr	Tyr	Pro	Glu	Leu	Tyr	85	90	95
Lys	Leu	Val	Thr	Gly	Lys	Glu	Pro	Thr	Arg	Arg	Phe	Ser	Thr	Ile	Val	100	105	110
Val	Glu	Glu	Gly	His	Glu	Gly	Leu	Thr	His	Phe	Leu	Met	Asn	Glu	Val	115	120	125
Ile	Lys	Leu	Gln	Gln	Gln	Met	Lys	Ala	Lys	Asp	Leu	Gln	Arg	Cys	Glu	130	135	140
Leu	Leu	Ala	Arg	Leu	Arg	Gln	Leu	Glu	Asp	Glu	Lys	Lys	Gln	Met	Thr	145	150	155
Leu	Thr	Arg	Val	Glu	Leu	Leu	Thr	Phe	Gln	Glu	Arg	Tyr	Tyr	Lys	Met	165	170	175
Lys	Glu	Glu	Arg	Asp	Ser	Tyr	Asn	Asp	Glu	Leu	Val	Lys	Val	Lys	Asp	180	185	190
Asp	Asn	Tyr	Asn	Leu	Ala	Met	Arg	Tyr	Ala	Gln	Leu	Ser	Glu	Glu	Lys	195	200	205
Asn	Met	Ala	Val	Met	Arg	Ser	Arg	Asp	Leu	Gln	Leu	Glu	Ile	Asp	Gln	210	215	220
Leu	Lys	His	Arg	Leu	Asn	Lys	Met	Glu	Glu	Glu	Cys	Lys	Leu	Glu	Arg	225	230	235
Asn	Gln	Ser	Leu	Lys	Leu	Lys	Asn	Asp	Ile	Glu	Asn	Arg	Pro	Lys	Lys	245	250	255
Glu	Gln	Val	Leu	Glu	Leu	Glu	Arg	Glu	Asn	Glu	Met	Leu	Lys	Thr	Lys	260	265	270
Asn	Gln	Glu	Leu	Gln	Ser	Ile	Ile	Gln	Ala	Gly	Lys	Arg	Ser	Leu	Pro	275	280	285
Asp	Ser	Asp	Lys	Ala	Ile	Leu	Asp	Ile	Leu	Glu	His	Asp	Arg	Lys	Glu	290	295	300
Ala	Leu	Glu	Asp	Arg	Gln	Glu	Leu	Val	Asn	Arg	Ile	Tyr	Asn	Leu	Gln	305	310	315
Glu	Glu	Ala	Arg	Gln	Ala	Glu	Glu	Leu	Arg	Asp	Lys	Tyr	Leu	Glu	Glu	325	330	335
Lys	Glu	Asp	Leu	Glu	Leu	Lys	Cys	Ser	Thr	Leu	Gly	Lys	Asp	Cys	Glu	340	345	350
Met	Tyr	Lys	His	Arg	Met	Asn	Thr	Val	Met	Leu	Gln	Leu	Glu	Glu	Val	355	360	365
Glu	Arg	Glu	Arg	Asp	Gln	Gly	Gln	Ala	Val	Ala	Phe	Gln	Gly	His	Cys	370	375	380
Ile	Lys	Ala	Leu	Asn	Thr	Glu	Pro	Ala	Thr	Ser	Lys	Gly	Arg	Thr	Ile	385	390	395
Gly	Ser	Val	Ile	Ala	Leu	Met	Lys	Lys	Ala	Phe	His	Ser	Arg	Asp	Glu	405	410	415
Ala	Gln	Thr	Gln	Tyr	Ser	Gln	Cys	Leu	Ile	Glu	Lys	Asp	Lys	Tyr	Arg	420	425	430
Lys	Gln	Ile	Arg	Glu	Leu	Glu	Glu	Lys	Asn	Asp	Glu	Met	Arg	Ile	Glu			

435		440		445
Met Val Arg Arg Glu Ala Cys Ile Val Asn Leu Glu Ser Lys Leu Arg				
450		455		460
Arg Leu Ser Lys Asp Ser Asn Asn Leu Asp Gln Ser Leu Pro Arg Asn				
465		470		480
Leu Pro Val Thr Ile Ile Ser Gln Asp Phe Gly Asp Ala Ser Pro Arg				
	485		490	495
Thr Asn Gly Gln Glu Ala Asp Asp Ser Ser Thr Ser Glu Glu Ser Pro				
	500		505	510
Glu Asp Ser Lys Tyr Phe Leu Pro Tyr His Pro Pro Gln Arg Arg Met				
	515		520	525
Asn Leu Lys Gly Ile Gln Leu Gln Arg Ala Lys Ser Pro Ile Ser Leu				
	530		535	540
Lys Arg Thr Ser Asp Phe Gln Ala Lys Gly His Glu Glu Glu Gly Thr				
545		550		560
Asp Ala Ser Pro Ser Ser Cys Gly Ser Leu Pro Ile Thr Asn Ser Phe				
	565		570	575
Thr Lys Met Pro Pro Arg Ser Arg Ser Ser Ile Met Ser Ile Thr Ala				
	580		585	590
Glu Pro Pro Gly Asn Asp Ser Ile Val Arg Arg Tyr Lys Glu Asp Ala				
	595		600	605
Pro His Arg Ser Thr Val Glu Glu Asp Asn Asp Ser Gly Gly Phe Asp				
	610		615	620
Ala Leu Asp Leu Asp Glu Leu Ala Ala Gly Glu Thr Val Ala Gln Ser				
625		630		640
Pro Pro Gly Val Pro Cys Gln Pro Pro Leu Phe Gln Gly Ser Pro Ser				
	645		650	655
Leu Cys Gln Leu Arg Leu Pro Thr Asp Glu Thr Lys Asp Glu Trp Ser				
	660		665	670
Ser Leu Met Gly Lys His Gln Arg Tyr Gln Val Leu Lys Arg Asp Asp				
	675		680	685
Ser His Glu Arg Tyr Ser Phe Gly Pro Ser Ser Ile His Ser Ser Ser				
	690		695	700
Ser Ser His Gln Ser Glu Gly Leu Asp Ala Tyr Asp Leu Glu Gln Val				
705		710		720
Asn Leu Met Phe Arg Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser				
	725		730	735
Val Thr Ser Val Gly His Val Arg Gly Pro Gly Pro Ser Val Gln His				
	740		745	750
Thr Thr Leu Asn Gly Asp Ser Leu Thr Ser Gln Leu Thr Leu Gly				
	755		760	765
Gly Asn Ala Arg Gly Ser Phe Val His Ser Val Lys Pro Gly Ser Leu				
	770		775	780
Ala Glu Lys Ala Gly Leu Arg Glu Gly His Gln Leu Leu Leu Glu				
785		790		800
Gly Cys Ile Arg Gly Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr				
	805		810	815
Lys Glu Glu Ala His Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr				
	820		825	830
Leu His Tyr Lys Val Asn His Glu Ala Gln Gln Lys Ile Arg Gly Pro				
	835		840	845
Ala Glu Tyr Asp Val Gly Ser Thr Ser Lys Ala Arg Ser Cys Ala Ala				
	850		855	860

Ala	Gln	Pro	Cys	Lys	Ser	Gly	Ile	Pro	Gly	Lys	Glu	Ser	Ser	Phe	Arg
865					870					875					880
Gln	Gly	Tyr	Arg	Lys	Leu	Val	Lys	Asp	Met	Glu	Asp	Gly	Leu	Ile	Thr
				885					890						895
Ser	Gly	Asp	Ser	Phe	Tyr	Ile	Arg	Leu	Asn	Leu	Asn	Ile	Ser	Ser	Gln
			900					905					910		
Leu	Asp	Ala	Cys	Thr	Met	Ser	Leu	Lys	Cys	Asp	Asp	Val	Val	His	Val
	915						920					925			
Arg	Asp	Thr	Met	Tyr	Gln	Asp	Arg	His	Glu	Trp	Leu	Cys	Ala	Arg	Val
930						935					940				
Asp	Pro	Phe	Thr	Asp	His	Asp	Leu	Asp	Met	Gly	Thr	Ile	Pro	Ser	Tyr
945					950					955					960
Ser	Arg	Ala	Gln	Gln	Leu	Leu	Leu	Val	Lys	Leu	Gln	Arg	Leu	Met	His
				965					970						975
Arg	Gly	Ser	Arg	Glu	Glu	Val	Asp	Gly	Thr	His	His	Thr	Leu	Arg	Ala
		980						985					990		
Leu	Arg	Phe	Val	Ser	Arg	Ser	Glu	Asn	Lys	Tyr	Lys	Arg	Met	Asn	Ser
	995						1000					1005			
Asn	Glu	Arg	Val	Arg	Ile	Ile	Ser	Gly	Ser	Pro	Leu	Gly	Ser	Leu	Ala
1010						1015					1020				
Arg	Ser	Ser	Leu	Asp	Ala	Thr	Lys	Leu	Leu	Thr	Glu	Lys	Gln	Glu	Glu
1025					1030					1035					1040
Leu	Asp	Pro	Glu	Ser	Glu	Leu	Gly	Lys	Asn	Leu	Ser	Leu	Ile	Pro	Tyr
				1045					1050						1055
Ser	Leu	Val	Arg	Ala	Phe	Tyr	Cys	Glu	Arg	Arg	Arg	Pro	Val	Leu	Phe
		1060						1065					1070		
Thr	Pro	Thr	Val	Leu	Ala	Lys	Thr	Leu	Val	Gln	Arg	Leu	Leu	Asn	Ser
	1075						1080					1085			
Gly	Gly	Ala	Met	Glu	Phe	Thr	Ile	Cys	Lys	Ser	Asp	Ile	Val	Thr	Arg
	1090					1095					1100				
Asp	Glu	Phe	Leu	Arg	Arg	Gln	Lys	Thr	Glu	Thr	Ile	Ile	Tyr	Ser	Arg
1105					1110					1115					1120
Glu	Lys	Asn	Pro	Asn	Ala	Phe	Glu	Cys	Ile	Ala	Pro	Ala	Asn	Ile	Glu
				1125					1130					1135	
Ala	Val	Ala	Ala	Lys	Asn	Lys	His	Cys	Leu	Leu	Glu	Ala	Gly	Ile	Gly
		1140						1145					1150		
Cys	Thr	Arg	Asp	Leu	Ile	Lys	Ser	Asn	Ile	Tyr	Pro	Ile	Val	Leu	Phe
	1155						1160					1165			
Ile	Arg	Val	Cys	Glu	Lys	Asn	Ile	Lys	Arg	Phe	Arg	Lys	Leu	Leu	Pro
	1170					1175					1180				
Arg	Pro	Glu	Thr	Glu	Glu	Phe	Leu	Arg	Val	Cys	Arg	Leu	Lys	Glu	
1185					1190					1195					1200
Lys	Glu	Leu	Glu	Ala	Leu	Pro	Cys	Leu	Tyr	Ala	Thr	Val	Glu	Pro	Asp
				1205					1210					1215	
Met	Trp	Gly	Ser	Val	Glu	Glu	Leu	Leu	Arg	Val	Val	Lys	Asp	Lys	Ile
		1220						1225					1230		
Gly	Glu	Glu	Gln	Arg	Lys	Thr	Ile	Trp	Val	Asp	Glu	Asp	Gln	Leu	
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<210> 9

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(276)

<400> 9

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Glu Asp Ala Leu Trp Glu Asn Val Glu Cys Asn Arg His Met Leu Ser	
1 5 10 15	
cgc tat atc aac cct gcc aag ctc acg ccc tac ctg cgt cag tgt aag	96
Arg Tyr Ile Asn Pro Ala Lys Leu Thr Pro Tyr Leu Arg Gln Cys Lys	
20 25 30	
gtc att gat gag cag gat gaa gat gaa gtg ctt aat gcc cct atg ctg	144
Val Ile Asp Glu Gln Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu	
35 40 45	
cca tcc aag atc aac cga gca ggc cgg ctg ttg gac att cta cat acc	192
Pro Ser Lys Ile Asn Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr	
50 55 60	
aag ggg caa agg ggc tat gtg gtc ttc ttg gag agc cta gaa ttt tat	240
Lys Gly Gln Arg Gly Tyr Val Val Phe Leu Glu Ser Leu Glu Phe Tyr	
65 70 75 80	
tac cca gaa ctg tac aaa ctg gtg act ggg aaa gag	276
Tyr Pro Glu Leu Tyr Lys Leu Val Thr Gly Lys Glu	
85 90	

<210> 10

<211> 92

<212> PRT

<213> Homo sapiens

<400> 10

Glu Asp Ala Leu Trp Glu Asn Val Glu Cys Asn Arg His Met Leu Ser	
1 5 10 15	
Arg Tyr Ile Asn Pro Ala Lys Leu Thr Pro Tyr Leu Arg Gln Cys Lys	
20 25 30	
Val Ile Asp Glu Gln Asp Glu Asp Glu Val Leu Asn Ala Pro Met Leu	
35 40 45	
Pro Ser Lys Ile Asn Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr	
50 55 60	
Lys Gly Gln Arg Gly Tyr Val Val Phe Leu Glu Ser Leu Glu Phe Tyr	
65 70 75 80	
Tyr Pro Glu Leu Tyr Lys Leu Val Thr Gly Lys Glu	
85 90	

<210> 11



<211> 957  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(957)

<400> 11

aag ctg cag cag cag atg aag gcc aag gac ctg caa cgc tgc gag ctg	48
Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu Leu	
1 5 10 15	
ctg gcc agg ttg cgg cag ctg gag gat gag aag aag cag atg acg ctg	96
Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr Leu	
20 25 30	
acg cgc gtg gag ctg cta acc ttc cag gag cgg tac tac aag atg aag	144
Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met Lys	
35 40 45	
gaa gag cgg gac agc tac aat gac gag ctg gtc aag gtg aag gac gac	192
Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp Asp	
50 55 60	
aac tac aac tta gcc atg cgc tac gca cag ctc agt gag gag aag aac	240
Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys Asn	
65 70 75 80	
atg gcg gtc atg agg agc cga gac ctc caa ctc gag atc gat cag cta	288
Met Ala Val Met Arg Ser Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu	
85 90 95	
aag cac cgg ttg aat aag atg gag gag gaa tgt aag ctg gag aga aat	336
Lys His Arg Leu Asn Lys Met Glu Glu Glu Cys Lys Leu Glu Arg Asn	
100 105 110	
cag tct cta aaa ctg aag aat gac att gaa aat cgg ccc aag aag gag	384
Gln Ser Leu Lys Leu Lys Asn Asp Ile Glu Asn Arg Pro Lys Lys Glu	
115 120 125	
cag gtt ctg gaa ctg gag cgg gag aat gaa atg ctg aag acc aaa aac	432
Gln Val Leu Glu Leu Glu Arg Glu Asn Glu Met Leu Lys Thr Lys Asn	
130 135 140	
cag gag ctg cag tcc atc atc cag gcc ggg aag cgc agc ctg cca gac	480
Gln Glu Leu Gln Ser Ile Ile Gln Ala Gly Lys Arg Ser Leu Pro Asp	
145 150 155 160	
tca gac aag gcc atc ctg gac atc ttg gaa cac gac cgc aag gag gcc	528
Ser Asp Lys Ala Ile Leu Asp Ile Leu Glu His Asp Arg Lys Glu Ala	
165 170 175	

ctg gag gac agg cag gag ctg gtc aac agg atc tac aac ctg cag gag	576
Leu Glu Asp Arg Gln Glu Leu Val Asn Arg Ile Tyr Asn Leu Gln Glu	
180 185 190	
gag gcc cgc cag gca gag gag ctg cga gac aag tac ctg gag gag aag	624
Glu Ala Arg Gln Ala Glu Glu Leu Arg Asp Lys Tyr Leu Glu Glu Lys	
195 200 205	
gag gac ctg gag ctc aag tgc tcg acc ctg gga aag gac tgt gaa atg	672
Glu Asp Leu Glu Leu Lys Cys Ser Thr Leu Gly Lys Asp Cys Glu Met	
210 215 220	
tac aag cac cgc atg aac acg gtc atg ctg cag ctg gag gag gtg gag	720
Tyr Lys His Arg Met Asn Thr Val Met Leu Gln Leu Glu Glu Val Glu	
225 230 235 240	
cgg gag cgg gac cag gga cag gct gtg gcc ttc cag gga cac tgc atc	768
Arg Glu Arg Asp Gln Gly Gln Ala Val Ala Phe Gln Gly His Cys Ile	
245 250 255	
aaa gct ctc aac aca gag cct gcc act agc aag ggt cgg acc atc ggc	816
Lys Ala Leu Asn Thr Glu Pro Ala Thr Ser Lys Gly Arg Thr Ile Gly	
260 265 270	
tct gtg atc gcg tta atg aag aag gcc ttc cac tcc cga gat gaa gct	864
Ser Val Ile Ala Leu Met Lys Lys Ala Phe His Ser Arg Asp Glu Ala	
275 280 285	
cag aca cag tac tcg cag tgc tta atc gaa aag gac aag tac agg aag	912
Gln Thr Gln Tyr Ser Gln Cys Leu Ile Glu Lys Asp Lys Tyr Arg Lys	
290 295 300	
cag atc cgc gag ctg gag gag aag aac gac gag atg agg atc gag	957
Gln Ile Arg Glu Leu Glu Glu Lys Asn Asp Glu Met Arg Ile Glu	
305 310 315	

<210> 12

<211> 319

<212> PRT

<213> Homo sapiens

<400> 12

Lys Leu Gln Gln Gln Met Lys Ala Lys Asp Leu Gln Arg Cys Glu Leu	
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Leu Ala Arg Leu Arg Gln Leu Glu Asp Glu Lys Lys Gln Met Thr Leu	
20 25 30	
Thr Arg Val Glu Leu Leu Thr Phe Gln Glu Arg Tyr Tyr Lys Met Lys	
35 40 45	
Glu Glu Arg Asp Ser Tyr Asn Asp Glu Leu Val Lys Val Lys Asp Asp	
50 55 60	
Asn Tyr Asn Leu Ala Met Arg Tyr Ala Gln Leu Ser Glu Glu Lys Asn	

65		70		75		80									
Met	Ala	Val	Met	Arg	Ser	Arg	Asp	Leu	Gln	Leu	Glu	Ile	Asp	Gln	Leu
			85					90						95	
Lys	His	Arg	Leu	Asn	Lys	Met	Glu	Glu	Glu	Cys	Lys	Leu	Glu	Arg	Asn
			100					105						110	
Gln	Ser	Leu	Lys	Leu	Lys	Asn	Asp	Ile	Glu	Asn	Arg	Pro	Lys	Lys	Glu
			115					120						125	
Gln	Val	Leu	Glu	Leu	Glu	Arg	Glu	Asn	Glu	Met	Leu	Lys	Thr	Lys	Asn
			130					135						140	
Gln	Glu	Leu	Gln	Ser	Ile	Ile	Gln	Ala	Gly	Lys	Arg	Ser	Leu	Pro	Asp
145								150						155	
Ser	Asp	Lys	Ala	Ile	Leu	Asp	Ile	Leu	Glu	His	Asp	Arg	Lys	Glu	Ala
								165						170	
Leu	Glu	Asp	Arg	Gln	Glu	Leu	Val	Asn	Arg	Ile	Tyr	Asn	Leu	Gln	Glu
			180											190	
Glu	Ala	Arg	Gln	Ala	Glu	Glu	Leu	Arg	Asp	Lys	Tyr	Leu	Glu	Glu	Lys
			195											200	
Glu	Asp	Leu	Glu	Leu	Lys	Cys	Ser	Thr	Leu	Gly	Lys	Asp	Cys	Glu	Met
			210											220	
Tyr	Lys	His	Arg	Met	Asn	Thr	Val	Met	Leu	Gln	Leu	Glu	Glu	Val	Glu
														235	
Arg	Glu	Arg	Asp	Gln	Gly	Gln	Ala	Val	Ala	Phe	Gln	Gly	His	Cys	Ile
														245	
Lys	Ala	Leu	Asn	Thr	Glu	Pro	Ala	Thr	Ser	Lys	Gly	Arg	Thr	Ile	Gly
														260	
Ser	Val	Ile	Ala	Leu	Met	Lys	Lys	Ala	Phe	His	Ser	Arg	Asp	Glu	Ala
														275	
Gln	Thr	Gln	Tyr	Ser	Gln	Cys	Leu	Ile	Glu	Lys	Asp	Lys	Tyr	Arg	Lys
														290	
Gln	Ile	Arg	Glu	Leu	Glu	Glu	Lys	Asn	Asp	Glu	Met	Arg	Ile	Glu	
														305	
														310	
														315	

<210> 13  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(339)

<400> 13	
aag ttc tct ctg gaa aga ccc ttc cgg cct tcg gtc acc tct gtg ggg	48
Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser Val Thr Ser Val Gly	
1 5 10 15	
cac gtg cgg ggc cca ggg ccc tcg gtg cag cac acg acg ctg aat ggc	96
His Val Arg Gly Pro Gly Pro Ser Val Gln His Thr Thr Leu Asn Gly	
20 25 30	
gac agc ctc acc tcc cag ctc acc ctg ctg ggg ggc aac gcg cga ggg	144
Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly	

35	40	45	
agc ttc gtg cac tcg gtc aag cct ggc tct ctg gcc gag aaa gcc ggc			192
Ser Phe Val His Ser Val Lys Pro Gly Ser Leu Ala Glu Lys Ala Gly			
50	55	60	
ctc cgt gag ggc cac cag ctg ctg ctg cta gaa ggc tgc atc cga ggc			240
Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu Gly Cys Ile Arg Gly			
65	70	75	80
gag agg cag agt gtc ccg ttg gac aca tgc acc aaa gag gaa gcc cac			288
Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr Lys Glu Glu Ala His			
85	90	95	
tgg acc atc cag agg tgc agc ggc ccc gtc acg ctg cac tac aag gtc			336
Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr Leu His Tyr Lys Val			
100	105	110	
aac			339
Asn			

<210> 14  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Lys Phe Ser Leu Glu Arg Pro Phe Arg Pro Ser Val Thr Ser Val Gly			
1	5	10	15
His Val Arg Gly Pro Gly Pro Ser Val Gln His Thr Thr Leu Asn Gly			
20	25	30	
Asp Ser Leu Thr Ser Gln Leu Thr Leu Leu Gly Gly Asn Ala Arg Gly			
35	40	45	
Ser Phe Val His Ser Val Lys Pro Gly Ser Leu Ala Glu Lys Ala Gly			
50	55	60	
Leu Arg Glu Gly His Gln Leu Leu Leu Leu Glu Gly Cys Ile Arg Gly			
65	70	75	80
Glu Arg Gln Ser Val Pro Leu Asp Thr Cys Thr Lys Glu Glu Ala His			
85	90	95	
Trp Thr Ile Gln Arg Cys Ser Gly Pro Val Thr Leu His Tyr Lys Val			
100	105	110	
Asn			

<210> 15  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(417)

<221> misc\_feature

<222> 416, 417

<223> n = A,T,C or G

<400> 15

atg ggg gaa ctg tgc cgc agg gac tcc gca ctc acg gca ctg gac gag	48
Met Gly Glu Leu Cys Arg Arg Asp Ser Ala Leu Thr Ala Leu Asp Glu	
1' 5 10 15	
gag aca ctg tgg gag atg atg gag agc cac cgc cac agg atc gta cgc	96
Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val Arg	
20 25 30	
tgc atc tgc ccc agc cgc ctc acc ccc tac ctg cgc cag gcc aag gtg	144
Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys Val	
35 40 45	
ctg tgc cag ctg gac gag gag gag gtg ctg cac agc ccc cgg ctc acc	192
Leu Cys Gln Leu Asp Glu Glu Glu Val Leu His Ser Pro Arg Leu Thr	
50 55 60	
aac agc gcc atg cgg gcc ggg cac ttg ctg gat ttg ctg aag act cga	240
Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr Arg	
65 70 75 80	
ggg aag aac ggg gcc atc gcc ttc ctg gag agc ctg aag ttc cac aac	288
Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His Asn	
85 90 95	
cct gac gtc tac acc ctg gtc acc ggg ctg cag cct gat gtt gac ttc	336
Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln Pro Asp Val Asp Phe	
100 105 110	
agt aac ttt agc ggt gag agc tcc gac ttt gac ggt ttg gca ggc act	384
Ser Asn Phe Ser Gly Glu Ser Ser Asp Phe Asp Gly Leu Ala Gly Thr	
115 120 125	
tct agg aac ctc agg ctc ctg gta acc cca gnn	417
Ser Arg Asn Leu Arg Leu Leu Val Thr Pro Xaa	
130 135	

<210> 16

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 139

<223> Xaa = Any Amino Acid

<400> 16

Met	Gly	Glu	Leu	Cys	Arg	Arg	Asp	Ser	Ala	Leu	Thr	Ala	Leu	Asp	Glu
1				5					10					15	
Glu	Thr	Leu	Trp	Glu	Met	Met	Glu	Ser	His	Arg	His	Arg	Ile	Val	Arg
		20						25					30		
Cys	Ile	Cys	Pro	Ser	Arg	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Ala	Lys	Val
	35						40					45			
Leu	Cys	Gln	Leu	Asp	Glu	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	Thr
	50					55					60				
Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	Arg
65					70					75					80
Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	Asn
			85						90					95	
Pro	Asp	Val	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Gln	Pro	Asp	Val	Asp	Phe
		100						105					110		
Ser	Asn	Phe	Ser	Gly	Glu	Ser	Ser	Asp	Phe	Asp	Gly	Leu	Ala	Gly	Thr
	115						120					125			
Ser	Arg	Asn	Leu	Arg	Leu	Leu	Val	Thr	Pro	Xaa					
	130					135									

<210> 17

<211> 276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(276)

<400> 17

gag	gag	aca	ctg	tgg	gag	atg	atg	gag	agc	cac	cgc	cac	agg	atc	gta	48
Glu	Glu	Thr	Leu	Trp	Glu	Met	Met	Glu	Ser	His	Arg	His	Arg	Ile	Val	
1				5					10					15		
cgc	tgc	atc	tgc	ccc	agc	cgc	ctc	acc	ccc	tac	ctg	cgc	cag	gcc	aag	96
Arg	Cys	Ile	Cys	Pro	Ser	Arg	Leu	Thr	Pro	Tyr	Leu	Arg	Gln	Ala	Lys	
			20					25					30			
gtg	ctg	tgc	cag	ctg	gac	gag	gag	gag	gtg	ctg	cac	agc	ccc	cgg	ctc	144
Val	Leu	Cys	Gln	Leu	Asp	Glu	Glu	Glu	Val	Leu	His	Ser	Pro	Arg	Leu	
		35					40					45				
acc	aac	agc	gcc	atg	cgg	gcc	ggg	cac	ttg	ctg	gat	ttg	ctg	aag	act	192
Thr	Asn	Ser	Ala	Met	Arg	Ala	Gly	His	Leu	Leu	Asp	Leu	Leu	Lys	Thr	
	50					55					60					
cga	ggg	aag	aac	ggg	gcc	atc	gcc	ttc	ctg	gag	agc	ctg	aag	ttc	cac	240
Arg	Gly	Lys	Asn	Gly	Ala	Ile	Ala	Phe	Leu	Glu	Ser	Leu	Lys	Phe	His	
65					70					75					80	

aac cct gac gtc tac acc ctg gtc acc ggg ctg cag 276  
Asn Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln  
85 90

<210> 18  
<211> 92  
<212> PRT  
<213> Homo sapiens

<400> 18  
Glu Glu Thr Leu Trp Glu Met Met Glu Ser His Arg His Arg Ile Val  
1 5 10 15  
Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro Tyr Leu Arg Gln Ala Lys  
20 25 30  
Val Leu Cys Gln Leu Asp Glu Glu Val Leu His Ser Pro Arg Leu  
35 40 45  
Thr Asn Ser Ala Met Arg Ala Gly His Leu Leu Asp Leu Leu Lys Thr  
50 55 60  
Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu Glu Ser Leu Lys Phe His  
65 70 75 80  
Asn Pro Asp Val Tyr Thr Leu Val Thr Gly Leu Gln  
85 90

<210> 19  
<211> 2176  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (147) ... (1247)

<400> 19  
atcatcagga agtgcacagg cgtccggcgt gctcctccct ccctgcagcc ccgggcagca 60  
tctcccagag gctccgcggc ccaggctcct ggtgtgtctg cagtgcaggt ggctcctgga 120  
agaccctcag cctgcctgct gaggcc atg tcg gac tac gag aac gat gac gag 173  
Met Ser Asp Tyr Glu Asn Asp Asp Glu  
1 5

tgc tgg aac gtc ctg gag ggc ttc cgg gtg acg ctc acc tcg gtc atc 221  
Cys Trp Asn Val Leu Glu Gly Phe Arg Val Thr Leu Thr Ser Val Ile  
10 15 20 25

gac ccc tca cgc atc aca cct tac ctg cgg cag tgc aag gtc ctg aac 269  
Asp Pro Ser Arg Ile Thr Pro Tyr Leu Arg Gln Cys Lys Val Leu Asn  
30 35 40

cct gat gat gag gag cag gtg ctc agc gac ccc aac ctg gtc atc cgc 317  
Pro Asp Asp Glu Glu Gln Val Leu Ser Asp Pro Asn Leu Val Ile Arg  
45 50 55

aaa cgg aaa gtg ggt gtg ctc ctg gac atc ctg cag cgg acc ggc cac	365
Lys Arg Lys Val Gly Val Leu Leu Asp Ile Leu Gln Arg Thr Gly His	
60 65 70	
aag ggc tac gtg gcc ttc ctc gag agc ctg gag ctc tac tac ccg cag	413
Lys Gly Tyr Val Ala Phe Leu Glu Ser Leu Glu Leu Tyr Tyr Pro Gln	
75 80 85	
ctg tac aag aag gtc aca ggc aag gag ccg gcc cgc gtc ttc tcc atg	461
Leu Tyr Lys Lys Val Thr Gly Lys Glu Pro Ala Arg Val Phe Ser Met	
90 95 100 105	
atc atc gac gcg tcc ggg gag tca ggc ctg act cag ctg ctg atg act	509
Ile Ile Asp Ala Ser Gly Glu Ser Gly Leu Thr Gln Leu Leu Met Thr	
110 115 120	
gag gtc atg aag ctg cag aag aag gtg cag gac ctg acc gcg ctg ctg	557
Glu Val Met Lys Leu Gln Lys Lys Val Gln Asp Leu Thr Ala Leu Leu	
125 130 135	
agc tcc aaa gat gac ttc atc aag gag ctg cgg gtg aag gac agc ctg	605
Ser Ser Lys Asp Asp Phe Ile Lys Glu Leu Arg Val Lys Asp Ser Leu	
140 145 150	
ctg cgc aag cac cag gag cgt gtg cag agg ctc aag gag gag tgc gag	653
Leu Arg Lys His Gln Glu Arg Val Gln Arg Leu Lys Glu Glu Cys Glu	
155 160 165	
gcc ggc agc cgc gag ctc aag cgc tgc aag gag gag aac tac gac ctg	701
Ala Gly Ser Arg Glu Leu Lys Arg Cys Lys Glu Glu Asn Tyr Asp Leu	
170 175 180 185	
gcc atg cgc ctg gcg cac cag agt gag gag aag ggc gcc gcg ctc atg	749
Ala Met Arg Leu Ala His Gln Ser Glu Glu Lys Gly Ala Ala Leu Met	
190 195 200	
cgg aac cgt gac ctg cag ctg gag att gac cag ctc aag cac agc ctc	797
Arg Asn Arg Asp Leu Gln Leu Glu Ile Asp Gln Leu Lys His Ser Leu	
205 210 215	
atg aag gcc gag gac gac tgc aag gtg gag cgc aag cac acg ctg aag	845
Met Lys Ala Glu Asp Asp Cys Lys Val Glu Arg Lys His Thr Leu Lys	
220 225 230	
ctc agg cac gcc atg gag cag cgg ccc agc cag gag ctg ctg tgg gag	893
Leu Arg His Ala Met Glu Gln Arg Pro Ser Gln Glu Leu Leu Trp Glu	
235 240 245	
ctg cag cag gag aag gcc ctg ctc cag gcc cgg gtg cag gag ctg gag	941
Leu Gln Gln Glu Lys Ala Leu Leu Gln Ala Arg Val Gln Glu Leu Glu	
250 255 260 265	
gcc tcc gtc cag gag ggg aag ctg gac agg agc agc ccc tac atc cag	989



Ala Ser Val Gln Glu Gly Lys Leu Asp Arg Ser Ser Pro Tyr Ile Gln  
270 275 280

gta ctg gag gag gac tgg cgg cag gcg ctg cgg gac cac cag gag cag 1037  
Val Leu Glu Glu Asp Trp Arg Gln Ala Leu Arg Asp His Gln Glu Gln  
285 290 295

gcc aac acc atc ttc tcc ctg cgc aag gac ctc cgc cag ggc gag gcc 1085  
Ala Asn Thr Ile Phe Ser Leu Arg Lys Asp Leu Arg Gln Gly Glu Ala  
300 305 310

cga cgc ctc cgg tgc atg gag gag aag gag atg ttc gag ctg cag tgc 1133  
Arg Arg Leu Arg Cys Met Glu Glu Lys Glu Met Phe Glu Leu Gln Cys  
315 320 325

ctg gca cta cgt aag gac tcc aag atg tac aag gac cgc atc gag gcc 1181  
Leu Ala Leu Arg Lys Asp Ser Lys Met Tyr Lys Asp Arg Ile Glu Ala  
330 335 340 345

atc ctg ctg cag atg gag gag gtc gcc att gag cgg gac cag agc aca 1229  
Ile Leu Leu Gln Met Glu Glu Val Ala Ile Glu Arg Asp Gln Ser Thr  
350 355 360

caa atg gag ggg ctg tga ccagcctccg cgcccagcgg cttgacgtcc 1277  
Gln Met Glu Gly Leu \*  
365

tccggagcct ctgcttgagg ttgggcggcc gggccgaggg cccagggcaa gcttggggcc 1337  
ctcactgagg gtcggccttg tgctgtcccg tcaggccata gccacgcggg aggagctgca 1397  
cgcacagcac gcccgggggc tgcaggagaa ggacgcgctg cgcaagcagg tgcgggagct 1457  
gggcgagaag gcggatgagc tgcagctgca ggtgttccag tgtgaggcgc agctactggc 1517  
cgtggagggc aggtcaggc ggcagcagct ggagacgctc gtcctgagct ccgacctgga 1577  
agatggctca cccaggaggt cccaggagct ctactcccc caggacctgg aggacacca 1637  
gctctcagac aaaggctgcc ttgccggcgg ggggagcccg aaacagccct ttgcagctct 1697  
gcaccaggag caggttttgc ggaaccccc tgacgcaggc ctgagcagcg gggagccgcc 1757  
cgagaaggag cggcggcgcc tcaaagagag ttttgagaac taccgcagga agcgcgccct 1817  
caggaagatg cagaaaggat ggcggcaggg ggaggaggac cgggagaaca ccacgggcag 1877  
cgacaacacc gacactgagg gctcctagcc gcagcagact tccccagacc gtcgctgact 1937  
tggcctggaa cgaggaatct ggtgccctga aaggcccagc cggactgccg ggcattgggg 1997  
ccgtttgtta agcggcactc attttgcgga ggccatgcgg gtgctacca ccccatgca 2057  
cacgccatct gtgtaacttc aggatctgtt ctgtttcacc atgtaacaca caatacatgc 2117  
atgcattgta ttagtggttag aaaacacagc tgcgtaaata aacagcacgg gtgaccgcc 2176

<210> 20

<211> 366

<212> PRT

<213> Homo sapiens

<400> 20

Met Ser Asp Tyr Glu Asn Asp Asp Glu Cys Trp Asn Val Leu Glu Gly  
1 5 10 15  
Phe Arg Val Thr Leu Thr Ser Val Ile Asp Pro Ser Arg Ile Thr Pro  
20 25 30

Tyr	Leu	Arg	Gln	Cys	Lys	Val	Leu	Asn	Pro	Asp	Asp	Glu	Glu	Gln	Val
	35						40					45			
Leu	Ser	Asp	Pro	Asn	Leu	Val	Ile	Arg	Lys	Arg	Lys	Val	Gly	Val	Leu
	50					55					60				
Leu	Asp	Ile	Leu	Gln	Arg	Thr	Gly	His	Lys	Gly	Tyr	Val	Ala	Phe	Leu
65					70					75					80
Glu	Ser	Leu	Glu	Leu	Tyr	Tyr	Pro	Gln	Leu	Tyr	Lys	Lys	Val	Thr	Gly
				85					90					95	
Lys	Glu	Pro	Ala	Arg	Val	Phe	Ser	Met	Ile	Ile	Asp	Ala	Ser	Gly	Glu
		100						105					110		
Ser	Gly	Leu	Thr	Gln	Leu	Leu	Met	Thr	Glu	Val	Met	Lys	Leu	Gln	Lys
	115						120					125			
Lys	Val	Gln	Asp	Leu	Thr	Ala	Leu	Leu	Ser	Ser	Lys	Asp	Asp	Phe	Ile
	130					135					140				
Lys	Glu	Leu	Arg	Val	Lys	Asp	Ser	Leu	Leu	Arg	Lys	His	Gln	Glu	Arg
145					150					155					160
Val	Gln	Arg	Leu	Lys	Glu	Glu	Cys	Glu	Ala	Gly	Ser	Arg	Glu	Leu	Lys
				165					170					175	
Arg	Cys	Lys	Glu	Asn	Tyr	Asp	Leu	Ala	Met	Arg	Leu	Ala	His	Gln	
		180					185						190		
Ser	Glu	Glu	Lys	Gly	Ala	Ala	Leu	Met	Arg	Asn	Arg	Asp	Leu	Gln	Leu
	195						200					205			
Glu	Ile	Asp	Gln	Leu	Lys	His	Ser	Leu	Met	Lys	Ala	Glu	Asp	Asp	Cys
	210					215					220				
Lys	Val	Glu	Arg	Lys	His	Thr	Leu	Lys	Leu	Arg	His	Ala	Met	Glu	Gln
225					230					235					240
Arg	Pro	Ser	Gln	Glu	Leu	Leu	Trp	Glu	Leu	Gln	Gln	Glu	Lys	Ala	Leu
				245					250					255	
Leu	Gln	Ala	Arg	Val	Gln	Glu	Leu	Glu	Ala	Ser	Val	Gln	Glu	Gly	Lys
		260						265					270		
Leu	Asp	Arg	Ser	Ser	Pro	Tyr	Ile	Gln	Val	Leu	Glu	Glu	Asp	Trp	Arg
	275						280					285			
Gln	Ala	Leu	Arg	Asp	His	Gln	Glu	Gln	Ala	Asn	Thr	Ile	Phe	Ser	Leu
	290					295					300				
Arg	Lys	Asp	Leu	Arg	Gln	Gly	Glu	Ala	Arg	Arg	Leu	Arg	Cys	Met	Glu
305					310					315					320
Glu	Lys	Glu	Met	Phe	Glu	Leu	Gln	Cys	Leu	Ala	Leu	Arg	Lys	Asp	Ser
				325					330					335	
Lys	Met	Tyr	Lys	Asp	Arg	Ile	Glu	Ala	Ile	Leu	Leu	Gln	Met	Glu	Glu
		340						345					350		
Val	Ala	Ile	Glu	Arg	Asp	Gln	Ser	Thr	Gln	Met	Glu	Gly	Leu		
	355						360					365			

<210> 21

<211> 281

<212> DNA

<213> Homo sapiens

<400> 21

gagaggctcc gcggccccagg ctctggtgt gtctgcagtg caggtggctc ctggaagacc 60  
ctcagcctgc ctgctgaggc catgtttgac tacgagaacg atgacgagtg ctggagcgtc 120  
ctggaggggt tccgggtgac gtcacctcg gtcacgcacc cctcacgcat cacaccttac 180

ctgcggcagt gcaaggtcct gaaccccgat gatgaggagc aggtgctcag cgaccccaac 240  
ctgggtcatcc gcaaacggaa agtgggtgtg ctctggaca t 281

<210> 22

<211> 734

<212> DNA

<213> Gallus gallus

<400> 22

gggacagcct gctccgcaag caccaagagc ggggtgcagaa gatgagggag gagagggaca 60  
gtctaagcaa ggagctgcgg aagtgcagg atgagaacta caacctggca atgagctatg 120  
ccagacagag cgaggagaag agcagtgcc tcatgaagaa cagggacctg ctctagaga 180  
ttgatagctt gaagcatagc ctcatgaagg ctgaggacga ctgcaaacta gagcgtaagc 240  
actcgatgaa actgaagcat gccatagaac aacgtccgag ccatgaagtg atgtgggaga 300  
tccagcagga gaaggagctg cttttggcca agaatacagga gctggagaac actcttcagg 360  
ttgccaggga acagaatttg gagacgagtc tctcccatga gactgtgcag aatgactgca 420  
gccagggtgct ggagcgccag gacctgctga acacctgta ccaccttcgc aaggagctgc 480  
gccaagccga ggtgcttcga gacaagttcg aggagtgcag ctgagccac gaggagctgt 540  
ccgagaagga gcggaggagg atgaaggact gctttgagcg ttaccgcagg aagcgcgccc 600  
tgcgagagc gcccgcgggc ccgcccgcgg gaggcgact gggagccgag caggggcagc 660  
gacaacacgg acaccgaggg cagctagggg ccggccgagc tttcgagttt gcagctggat 720  
ccgtcaataa acag 734

<210> 23

<211> 630

<212> DNA

<213> Gallus gallus

<400> 23

tgaacaccct gtaccacctt cgcaaggagc tgcgccagc cgaggtgctc cgagacaagt 60  
atgcagagga aaaagaaata cttgaactac agtgcacatc tctgaggaag gactcccaga 120  
tgtataaaaa acggatggaa gctgtcttag agcagatgga ggaagtggct tcggaaagag 180  
accaggcact gctgaccaga gaacagttct acccacagta ctccaagaac cttgttgaga 240  
gggacactta tcggaagcag attcgggagc tgggggagcg atgcatgag ctgcagctgc 300  
agctcttcca aaaggagggt cagctactgg ctactgaagc caagctgaaa agactgcaac 360  
tggagctgcc tgcactgact tctgacctgg atgacctcc tccagagatc ccaggtctta 420  
ctctcatggt catctagacg aagatcgac ctgactaaaa aagacgctgt taaggaaaac 480  
cagcaatcag catgcaagaa acatctgacg cagatcacca cttcgaggat gcactaacca 540  
caagacttcg agaagacgga gagataagga tgcttgagcg tacgagtcgg ccgatccgcg 600  
ccccccctcc gcgctccttc cgtggctcgt 630

<210> 24

<211> 331

<212> DNA

<213> Homo sapiens

<400> 24

cacgagggaa atgtacaagc accgcatgaa cacggctcatg ctgcacctgg aggaggtgga 60  
gcgggagcgg gaccaggcct tccactccc agatgaagct cagacacagt actcgagtg 120  
cttaatcgaa aaggacaagt acaggaagca gatccgcgag ctggaggaga agaacgacga 180  
gatgaggatc gagatggtgc ggcgggaggc ctgcatcgtc aacctggaga gcaagctgcg 240  
gcgcctctcc aaggacagca acaacctgga ccagagtctg cccaggaacc tgccagtaac 300  
catcatctct caggactttg gggatgccag c 331

<210> 25  
<211> 478  
<212> DNA  
<213> Homo sapiens

<400> 25  
ttttttttttt tttttctctc ctgcctcctc tggccttcgg actcctgccc gcgcgcgccg 60  
cagccccctc cgggccctgc agccccctgg cgggcggcgc ccctcggagg acggctccgg 120  
gcccggggggg acggaggggc tggtcgcctg gaggaagccg gaggcctgcg tggaggaggc 180  
gccccgcgca gctggctggc ggagcatgag cgccccagat cccaagcact gcaagtccag 240  
atgcaacggg agcctggctc aagggacgac aagatccagc cggaaagtgt agaagtcaca 300  
ccccaatggc gggatagcag cccctgtgtg tgagcacccc tccatgccag gaggagggcc 360  
agagatggat gactacatgg agaccctgaa ggatgaagag gacccttgt gggacaatgt 420  
ggagtytaac cggcacatgc tcaaccgcta tatcaaccct gccaaagtca cgcctac 478

<210> 26  
<211> 396  
<212> DNA  
<213> Homo sapiens

<400> 26  
gcagccccct cccggccctg cagccccctg cgtgcggcgc catcggagga cggctccggg 60  
cccgggggga cggagggcct ggtcgcctgg aggaagccgg acgctgcgtg gaggaggcgc 120  
ccccgggtctg gtctggcgga cgatgagcgc ccagatccc aagcactgca agtccagatg 180  
caacggggagc ctggctcaag ggacgacaag atccagccgg aaagtgtaga agtcacaccc 240  
caatggcggg atagcagccc ctgtgtgtga tcacccctcc atgccaggag gagggccaga 300  
gatggatgac tacatggaga cgctgaatga tgaagaggac gccttgtggg agaattgtgga 360  
gtgtaaccgg cacatgctca gccgctatat caaccc 396

<210> 27  
<211> 162  
<212> DNA  
<213> Homo sapiens

<400> 27  
aaaaggagga gggccagaga tggatgacta catggagacg ctgaaggatg aagaggacgc 60  
cttgtgggtg aatgtggagt gtaaccggca catgctcagc cgggtctcac gaattccgct 120  
gagttctcac gaattccgct gaggtctcac gaattccgct ga 162

<210> 28  
<211> 418  
<212> DNA  
<213> Homo sapiens

<400> 28  
cacgacgacg gacgccagcc ctagctcctg cggatctctg cccatcacca actccttcac 60  
caagatgcag cccccccgga gccgcagcag catcatgtca atcaccgccg agccccggg 120  
aaacgactcc atcgtcagac gctacaagga ggacgcgcc catcgcagca cagtccaaga 180  
agacaatgac agcggggggg ttgacgcctt agatctggat gatgacagtc acgaacgcta 240  
ctccttcgga cctcctcca tccactcctc ctctcctcc caccaatccg agggcctgga 300  
tgctacgac ctggagcagg tcaacctcat gttcaggaag ttctctctgg aaagaccctt 360  
ccggccttcg gtcacctctg tggggcacgt tcggggccca aggcctcgg tgcagcac 418

<210> 29  
<211> 610  
<212> DNA  
<213> Homo sapiens

<400> 29  
tcattccccta cagcctggta cgcgccttct actgcgagcg ccgccggccc gtgctcttca 60  
caccacccgt gctggccaag acgctgggtg agaggctgct caactcggga ggtgccatgg 120  
agttcaccat ctgcaagtca gatatcgtca caagagatga gttcctcaga aggcagaaga 180  
cggagaccat catctactcc cgagagaaga accccaacgc gttcgaatgc atcgcccctg 240  
ccaacatcga agctgtggcc gccaaagaaca agcactgcct gctggaggct gggatcggct 300  
gcacaagaga cttgatcaag tccaacatct accccatcgt gctcttcac cgggtgtgtg 360  
agaagaacat caagagggtc agaaagctgc tgccccgacc tgagacggag gaggagtcc 420  
tgcgctgtg cgggctgaag gagaaggagc tggaggccct gccgtgctg tacgccacgg 480  
tggaacctga catgtggggc agcgtagagg agctgctccg cgttgtcaag gacaagatcg 540  
gcgaggagca gcgcaagacc atctgggtgg acgaggacca gctgtgaggc gggcgccctg 600  
ggcagagaga 610

<210> 30  
<211> 556  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 470  
<223> n = A,T,C or G

<400> 30  
tcattccccta cagcctggta cgcgccttct actgcgagcg ccgccggccc gtgctcttca 60  
caccacccgt gctggccaag acgctgggtg agaggctgct caactcggga ggtgccatgg 120  
agttcaccat ctgcaagtca gatatcgtca caagagatga gttcctcaga aggcagaaga 180  
cggagaccat catctactcc cgagagaaga accccaacgc gttcgaatgc atcgcccctg 240  
ccaacatcga agctgtggcc gccaaagaaca agcactgcct gctggaggct gggatcggct 300  
gcacaagaga cttgatcaag tccaacatct accccatcgt gctcttcac cgggtgtgtg 360  
agaagaacat caagagggtc agaaagctgc tgccccgacc tgagacggag gaggagtcc 420  
tgcgctgtg cgggctgaag gagaaggagc tggaggccct gccgttgccn tggtagcca 480  
cgggtggaacc tgacatgtgg ggcagcgtag aggagctgct ccgcgtgtca ggacagacgg 540  
cgagagcagc gcaaga 556

<210> 31  
<211> 390  
<212> DNA  
<213> Homo sapiens

<400> 31  
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ggtccgatca tctcggggag tccgctagga gcctggcccc gtctctgctg gacgccacca 120  
agctcttgac tgagaagcag gaagagctgg accctgagag cgagctgggc aagaacctca 180  
gcctcatccc ctacagcctg gtacgcgcct tctactgcga gcgcgcgcgg cctgtgctct 240  
tcacaccac cgtgctggcc aagacgctgg tgcaagggt gctcaactcg ggagggtcca 300  
tggagtccac catctgcaag tcagatatcg tcacaagaga tgagttctc agaaggcaga 360

agacggagac catcatctac tcccagagaga

390

<210> 32

<211> 620

<212> DNA

<213> Homo sapiens

<400> 32

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aacatcaaga ggttcagaaa gctgctgccc cggcctgaga cggaggagga gttcctgctc 120
gtgtgccggc tgaaggagaa ggagctggag gccctgccgt gcctgtacgc cacgggtgaa 180
cctgacatgt ggggcagcgt agaggagctg ctccgcgttg tcaaggacaa gatcggcgag 240
gagcagcgca agaccatctg ggtggacgag gaccagctgt gaggcgggcg ccctgggcag 300
agagactctg tggcgcgggg catcctatga ggcaggcacc ctgggcagag agatgtagtg 360
ggtgcggggg gatcctgttg cccacagagc tgcccagca gacgctccgc cccaccgggt 420
gatggagccc cggggggaca gtcgtgcctg gggaggagca gggtagagc cattccccca 480
gccctggtg acctggccta gcagttttgg cctgctggc cttagcaggg agacagggga 540
gcaaagaacg ccaagccggg aggcccaagc cagccgggct ctcgaggggg ggcccgggtc 600
ccattttgcc ctttatgagc                                     620
```

<210> 33

<211> 283

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> 42, 85, 109, 111, 139, 222, 244, 263

<223> n = A,T,C or G

<400> 33

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agaacatcaa gaggttcaga aagcngctgc cccggcctga gacggaggng nagttcctgc 120
gcgtgtgccg gctgaaggng aaggagctgg aggccttgcc gtgcctgtac gcgacgggtg 180
aacctgacat gtggggcagc gtagaggagc tgctccgcgt tntataagga caagatcggg 240
gagnagcagc gcaagaccat ctnggtagac gaggaccagc ttt                                     283
```

<210> 34

<211> 207

<212> DNA

<213> Homo sapiens

<400> 34

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gtgtactgcc ttctgaggaa ctcatctctg tgacgatata tgacttgagc atggtgaact 60
ccatggcacc tcccagattg agcagcctct gcaccagcgt cttggccagc acggtgggtg 120
tgaagagcac gggcggggcg cgctcgagc agaaggcgcg taccaggctg taggggatga 180
ggctgagggt cttgcccagc tcgtctct                                     207
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<210> 35

<211> 192

<212> DNA

<213> Homo sapiens

<400> 35  
gacttgatca agtccaacat ctaccccatc gtgctcttca tccgggtgtg tgagaagaac 60  
atcaagaggt tcagaaagct gctgccccgg cctgagactg gaggaggagt tcctgcgcgt 120  
gtgccggctg aaggagaagg agctggaggc cctgcgatgc ctgtacgcca cgggtggaacc 180  
tgacatgtgg gg 192

<210> 36  
<211> 605  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> 213  
<223> n = A,T,C or G

<400> 36  
gaaataataa tacattttta tgcaagagaa atcatagcct ggtacacacc ccttccccga 60  
tctgtcctgc ctggggatgt gtttatgggt agtgtgtccc caggactggg agtcacctgg 120  
ctgtccgggt ccccgcccta ctggcggcag catgcctgtc ccagcatta cattcaactg 180  
ctgctctggc tctcgagagg cgggtggcc tcnngccttc cggcttggcg ttctttgtc 240  
ccctgtctcc ctgctaaggc cagcagggcc aaactgctag gccaggtcag ccagggtgg 300  
gggaatgggc tgtacctgc tctccccag gcacgactgt cccccgggg ctccatcacc 360  
gggtggggcg gagcgtctgc tggggcagct ctgtgggcca caggatcccc ccgcacccac 420  
tgcctctctc tgcccatggg gctgctctca taggatgccc cgcgccacag agtctatatg 480  
tccagggcgc ccgctcaca gctggctctc gtccaccag atggtcttgc gctgtcctc 540  
gocgatcttg tcttgacat cgcggagcag ctcttttac ctgccccaca tgtcagggtg 600  
ccccg 605

<210> 37  
<211> 1141  
<212> DNA  
<213> Homo sapiens

<400> 37  
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tgggcttttg agacactgcg gggactgtgg accccacct gctgcacgga gctcctgcaa 120  
aagcaaacct gagaaccttg ggtcctccca gcgcccagcc atgggggaac tgtgccgcag 180  
ggactccgca ctacggcac tggacgagga gacactgtgg gagatgatgg agagccaccg 240  
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gcgccagagg ctggctgctg accatggatg gaccgaggag ggaggttget gcaccagcgc 360  
ccacgagaca tcaacaacag acgcacactg cggggccggg cacatagcgt ggcctcgcgc 420  
tagaaagaca tcagaggaga aagaagcggg ggcccactcg cactcacctg gagtagacgc 480  
catgcacagt accaccaaac ccatgagcgc tactacaacc catgggtcac cagggcatga 540  
cagcctggat gcatagacat aacaagtaac ttctactagc caggtcctca tgcgaagacc 600  
atcccagcc tgaccgcaca tgccctggac atggggccca ctacgcgcag accatgcagc 660  
gagagacgca tgacaccagg caacaacgcg ggccacgaac gcgagcgttg cctgcatcga 720  
cgggcacggt tggccacaga caggaattg cagcggagcc acacgtggca gcccctgagg 780  
cccgcagaca cccggtgcac cgaaggggccc atggcaacca cgacctggca ggcttgacac 840  
accaagcgc ataccacgcg cgtgaaaggg tacagaggca ccaactaccc agtgcaagcg 900  
cagttcttgc aaggcgatgc caaggaacg gcacgacatg acgacaccgc agtactctgt 960  
gaggaaacca tcttagcaag atgacagcct tgacaggaaa caacgacag aagtgcctgt 1020  
ctcgcaacgc atgacagaag acctgtcgca tataaagtaa atgtgatact aatagaaagc 1080

aagaagggttg acactgaaag acacacatat gagtataact cgagtatgca acgtgaacat 1140  
g 1141